

P1009PC00

1

SEQUENCE LISTING

<110> M&E Biotech A/S

<120> Novel Method For Down-Regulation Of Amyloid

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<170> PatentIn Ver. 3.0

<210> 1

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<212> DNA

<213> Homo sapiens

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<222> (1)..(2313)

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<221> misc\_feature

<222> (2098)..(2169)

<223> nucleotides encoding transmembrane region

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<222> (2014)..(2313)

<223> Nucleotides encoding C-100

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<222> (2016)..(2144)

<223> Abeta 42/43

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&lt;222&gt; (2014)..(2142)

&lt;223&gt; Abeta 42/43

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1				5					10					15		

gcg	ctg	gag	gta	ccc	act	gat	ggt	aat	gct	ggc	ctg	ctg	gct	gaa	ccc	96
Ala	Leu	Glu	Val	Pro	Thr	Asp	Gly	Asn	Ala	Gly	Leu	Leu	Ala	Glu	Pro	
			20					25					30			

cag	att	gcc	atg	ttc	tgt	ggc	aga	ctg	aac	atg	cac	atg	aat	gtc	cag	144
Gln	Ile	Ala	Met	Phe	Cys	Gly	Arg	Leu	Asn	Met	His	Met	Asn	Val	Gln	
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aat	ggg	aag	tgg	gat	tca	gat	cca	tca	ggg	acc	aaa	acc	tgc	att	gat	192
Asn	Gly	Lys	Trp	Asp	Ser	Asp	Pro	Ser	Gly	Thr	Lys	Thr	Cys	Ile	Asp	
	50					55					60					

acc	aag	gaa	ggc	atc	ctg	cag	tat	tgc	caa	gaa	gtc	tac	cct	gaa	ctg	240
Thr	Lys	Glu	Gly	Ile	Leu	Gln	Tyr	Cys	Gln	Glu	Val	Tyr	Pro	Glu	Leu	
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Gln	Ile	Thr	Asn	Val	Val	Glu	Ala	Asn	Gln	Pro	Val	Thr	Ile	Gln	Asn	
			85					90						95		

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Trp	Cys	Lys	Arg	Gly	Arg	Lys	Gln	Cys	Lys	Thr	His	Pro	His	Phe	Val	
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att	ccc	tac	cgc	tgc	tta	gtt	ggt	gag	ttt	gta	agt	gat	gcc	ctt	ctc	384
Ile	Pro	Tyr	Arg	Cys	Leu	Val	Gly	Glu	Phe	Val	Ser	Asp	Ala	Leu	Leu	
		115					120					125				

gtt	cct	gac	aag	tgc	aaa	ttc	tta	cac	cag	gag	agg	atg	gat	gtt	tgc	432
Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys	
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T00220-6T00220-60

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Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu	
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Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile	
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gac	aag	ttc	cga	ggg	gta	gag	ttt	gtg	tgt	tgc	cca	ctg	gct	gaa	gaa	576
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu	
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agt	gac	aat	gtg	gat	tct	gct	gat	gcg	gag	gag	gat	gac	tcg	gat	gtc	624
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val	
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tgg	tgg	ggc	gga	gca	gac	aca	gac	tat	gca	gat	ggg	agt	gaa	gac	aaa	672
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys	
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gta	gta	gaa	gta	gca	gag	gag	gaa	gaa	gtg	gct	gag	gtg	gaa	gaa	gaa	720
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu	
225					230					235					240	
gaa	gcc	gat	gat	gac	gag	gac	gat	gag	gat	ggg	gat	gag	gta	gag	gaa	768
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu	
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gag	gct	gag	gaa	ccc	tac	gaa	gaa	gcc	aca	gag	aga	acc	acc	agc	att	816
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile	
			260					265					270			
gcc	acc	acc	acc	acc	acc	acc	aca	gag	tct	gtg	gaa	gag	gtg	gtt	cga	864
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	
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gag	gtg	tgc	tct	gaa	caa	gcc	gag	acg	ggg	ccg	tgc	cga	gca	atg	atc	912
Glu	Val	Cys	Ser	Glu	Gln	Ala	Glu	Thr	Gly	Pro	Cys	Arg	Ala	Met	Ile	
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Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr	
325 330 335	
tgc atg gcc gtg tgt ggc agc gcc atg tcc caa agt tta ctc aag act	1056
Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr	
340 345 350	
acc cag gaa cct ctt gcc cga gat cct gtt aaa ctt cct aca aca gca	1104
Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala	
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gcc agt acc cct gat gcc gtt gac aag tat ctc gag aca cct ggg gat	1152
Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp	
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Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala	
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aag cac cga gag aga atg tcc cag gtc atg aga gaa tgg gaa gag gca	1248
Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala	
405 410 415	
gaa cgt caa gca aag aac ttg cct aaa gct gat aag aag gca gtt atc	1296
Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile	
420 425 430	
cag cat ttc cag gag aaa gtg gaa tct ttg gaa cag gaa gca gcc aac	1344
Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn	
435 440 445	
gag aga cag cag ctg gtg gag aca cac atg gcc aga gtg gaa gcc atg	1392
Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met	
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gat gcc cgc cct gct gcc gac cga gga ctg acc act cga cca ggt tct	1968
Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser	
645                                  650                                  655	
ggg ttg aca aat atc aag acg gag gag atc tct gaa gtg aag atg gat	2016
Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp	
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gca gaa ttc cga cat gac tca gga tat gaa gtt cat cat caa aaa ttg	2064
Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu	
675                                  680                                  685	
gtg ttc ttt gca gaa gat gtg ggt tca aac aaa ggt gca atc att gga	2112
Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly	
690                                  695                                  700	
ctc atg gtg ggc ggt gtt gtc ata gcg aca gtg atc gtc atc acc ttg	2160
Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu	
705                                  710                                  715                                  720	
gtg atg ctg aag aag aaa cag tac aca tcc att cat cat ggt gtg gtg	2208
Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val	
725                                  730                                  735	
gag gtt gac gcc gct gtc acc cca gag gag cgc cac ctg tcc aag atg	2256
Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met	
740                                  745                                  750	
cag cag aac ggc tac gaa aat cca acc tac aag ttc ttt gag cag atg	2304
Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met	
755                                  760                                  765	
cag aac tag	2313
Gln Asn	
770	

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Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Ala Arg  
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Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro  
20 25 30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln  
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Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp  
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Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu  
65 70 75 80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn  
85 90 95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val  
100 105 110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu  
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Val	Pro	Asp	Lys	Cys	Lys	Phe	Leu	His	Gln	Glu	Arg	Met	Asp	Val	Cys
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Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu  
145                      150                      155                      160

Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile  
165 170 175

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Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu  
180 185 190

Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val  
195 200 205

Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys  
210 215 220

Val Val Glu Val Ala Glu Glu Glu Glu Val Ala Glu Val Glu Glu Glu  
225 230 235 240

Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu  
245 250 255

Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile  
260 265 270

Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg  
275 280 285

Glu Val Cys Ser Glu Gln Ala Glu Thr Gly Pro Cys Arg Ala Met Ile  
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Ser Arg Trp Tyr Phe Asp Val Thr Glu Gly Lys Cys Ala Pro Phe Phe  
305 310 315 320

Tyr Gly Gly Cys Gly Gly Asn Arg Asn Asn Phe Asp Thr Glu Glu Tyr  
325 330 335

Cys Met Ala Val Cys Gly Ser Ala Met Ser Gln Ser Leu Leu Lys Thr  
340 345 350

Thr Gln Glu Pro Leu Ala Arg Asp Pro Val Lys Leu Pro Thr Thr Ala  
355 360 365

Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp  
370 375 380



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Glu Asn Glu His Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala  
385 390 395 400

Lys His Arg Glu Arg Met Ser Gln Val Met Arg Glu Trp Glu Glu Ala  
405 410 415

Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp Lys Lys Ala Val Ile  
420 425 430

Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn  
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Glu Arg Gln Gln Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met  
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Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu  
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Gln Ala Val Pro Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys  
485 490 495

Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe  
500 505 510

Glu His Val Arg Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser  
515 520 525

Gln Val Met Thr His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser  
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Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp  
545 550 555 560

Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val  
565 570 575

Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala  
580 585 590

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Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr Val Glu Leu Leu Pro  
595 600 605

Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe  
610 615 620

Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn Glu Val Glu Pro Val  
625 630 635 640

Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser  
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Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp  
660 665 670

Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu  
675 680 685

Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly  
690 695 700

Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr Leu  
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Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val  
725 730 735

Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met  
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Gln Asn  
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<222> (1)..(45)

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<212> PRT

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<223> DNA encoding P30 epitope

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12

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63

Ala Ser His Leu Glu

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<213> Clostridium tetani

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5

10

15

Ala Ser His Leu Glu

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&lt;213&gt; Synthetic

&lt;400&gt; 10

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&lt;212&gt; DNA

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&lt;213&gt; Synthetic

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